

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application.

**Listing of Claims:**

Claims 1-51. (canceled)

52. (currently amended) A method for processing fragment analysis data comprising:

Receiving the fragment analysis data wherein the data represents intensity values and nucleic acid fragment length information,

Determining the peaks of the fragment analysis data and forming a signal envelope from said peaks,

Determining the minima and maxima of the signal envelope and dividing the signal envelope into panels with boundaries at each local minimum,

Determining if at least three panels exist, and if so,

Computing an energy value for each panel,

Performing a first test by computing a first ratio of the energy value in the panel with the second greatest energy value to the energy value in the panel with the greatest energy value and determining if the first ratio exceeds a first threshold and if so, the first test is considered a pass,

Performing a second test by computing a second ratio of the energy value in the panel with the third greatest energy value to the energy value in the panel with the second greatest energy value and determining if the second ratio exceeds a second threshold and if so, the second test is considered a pass,

Calling alleles in each of the first and second panels if the first and second tests are passed, and

Reporting the allele calls to a user.

53. (previously presented) The method of claim 52 wherein said calling alleles step comprises:

Defining a first allele in the panel with the greatest energy value as the fragment length corresponding to the maximum intensity value in the first panel, and

Defining a second allele in the panel with the second greatest energy value as the fragment length corresponding to the maximum intensity value in the second panel.

54. (previously presented) The method of claim 52 wherein the energy value is defined by summing the square of the signal envelope contained in the panel.

55. (currently amended) A computer readable medium containing instructions for controlling a computer system to perform a method of processing fragment analysis data, the method comprising:

Receiving the fragment analysis data wherein the data represents intensity values and nucleic acid fragment length information,

Determining the peaks of the fragment analysis data and forming a signal envelope from said peaks,

Determining the minima and maxima of the signal envelope and dividing the signal envelope into panels with boundaries at each local minimum,

Determining if at least three panels exist, and if so,

Computing an energy value for each panel,

Performing a first test by computing a first ratio of the energy value in the panel with the second greatest energy value to the energy value in the panel with the greatest energy value and determining if the first ratio exceeds a first threshold and if so, the first test is considered a pass,

Performing a second test by computing a second ratio of the energy value in the panel with the third greatest energy value to the energy value in the panel with the second greatest energy value and determining if the second ratio exceeds a second threshold and if so, the second test is considered a pass,

Calling alleles in each of the first and second panels if the first and second tests are passed, and

Reporting the allele calls to a user.

56. (previously presented) The computer readable medium of claim 55 wherein said calling alleles step comprising:

Defining a first allele in the panel with the greatest energy value as the fragment length corresponding to the maximum intensity value in the first panel, and

Defining a second allele in the panel with the second greatest energy value as the fragment length corresponding to the maximum intensity value in the second panel.

57. (previously presented) The computer readable medium of claim 55 wherein the energy is defined by summing the square of the signal contained in the panel.